



# results of BLAST

## BLASTP 2.2.9 [May-01-2004]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1085452435-15497-118616244323.BLASTQ3

### Query=

(16 letters)

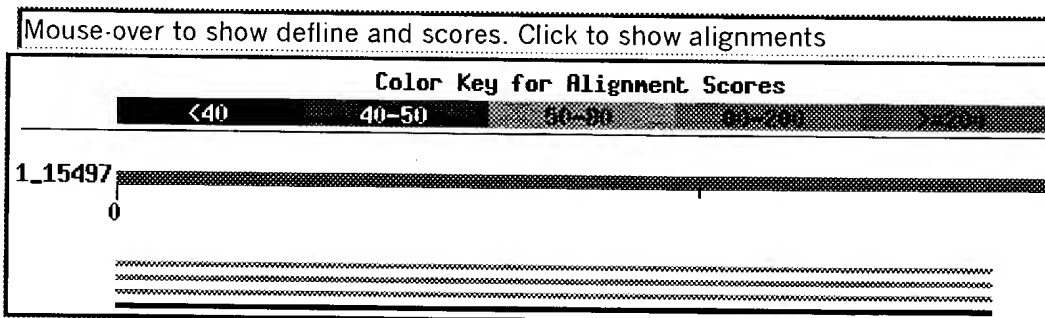
### Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples  
1,837,236 sequences; 608,447,635 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 653 Blast Hits on the Query Sequence























Sequences producing significant alignments:

#77

Score E  
(bits) Value

gi 601931 gb AAA57153.1  neurofilament-H	51	3e-06	
gi 226213 prf 1501343A neurofilament protein NF-H C term	51	3e-06	
gi 33302611 sp P12036 NFH_HUMAN Neurofilament triplet H pro...	51	3e-06	
gi 27529742 dbj BAA74868.2  KIAA0845 protein [Homo sapiens]	51	3e-06	
gi 284668 pir B43427 neurofilament protein H form H2 (repe...	51	3e-06	
gi 284667 pir A43427 neurofilament triplet H1 protein - ra...	51	3e-06	
gi 14250426 gb AAH08648.1  Unknown (protein for IMAGE:38662...	51	3e-06	
gi 108359 pir S02571 neurofilament triplet protein H - pig...	51	3e-06	
gi 24020878 gb AAN40837.1  heavy neurofilament protein [Can...	51	3e-06	

gi 71549 pir QFHUH	neurofilament triplet H protein - human...	51	3e-06	
gi 32483416 ref NP_066554.2	neurofilament, heavy polypepti...	51	3e-06	
gi 29789026 ref NP_036739.1	neurofilament, heavy polypepti...	47	3e-05	
gi 21429606 gb AAM49796.1	heavy neurofilament NF-H [Rattus...	47	3e-05	
gi 205686 gb AAA41695.1	heavy neurofilament subunit	47	3e-05	
gi 205680 gb AAA41692.1	high molecular weight neurofilament	47	3e-05	
gi 92538 pir S02003	neurofilament triplet H protein - rat ...	44	3e-04	
gi 46275814 ref NP_035034.1	neurofilament, heavy polypepti...	44	3e-04	
gi 128127 sp P19246 NFH_MOUSE	Neurofilament triplet H prote...	44	3e-04	
gi 28972433 dbj BAC65670.1	mKIAA0845 protein [Mus musculus]	44	3e-04	
gi 462702 sp P16884 NFH_RAT	Neurofilament triplet H protein...	44	3e-04	
gi 463250 emb CAA83229.1	Neurofilament protein, high molec...	44	3e-04	
gi 7428714 pir QFPGM	neurofilament triplet M protein - pig...	35	0.23	
gi 33468430 emb CAD70271.1	Secp1 protein precursor [Tricho...	32	1.0	
gi 39586313 emb CAE66724.1	Hypothetical protein CBG12070 [...	32	1.8	
gi 13629976 sp O77788 NFM_BOVIN	Neurofilament triplet M pro...	32	1.8	
gi 1160355 gb AAB00542.1	UNC-89	31	3.3	
gi 7511618 pir T29757	protein UNC-89 - Caenorhabditis elegans	31	3.3	
gi 31209313 ref XP_313623.1	ENSANGP00000013035 [Anopheles ...	31	3.3	
gi 31746683 gb AAP68958.1	Uncoordinated protein 89, isoform...	31	3.3	
gi 25141314 ref NP_491290.2	UNCordinated locomotion UNC-8...	31	3.3	
gi 2135810 pir I53671	neurofilament heavy subunit - human ...	30	4.4	
gi 39589705 emb CAE66940.1	Hypothetical protein CBG12332 [...	29	8.0	
gi 42521813 ref NP_967193.1	TonB-like protein [Bdellovibri...	29	8.0	
gi 19075023 ref NP_586624.1	similarity to GLYPICAN-4 (HEPA...	29	14	
gi 14549637 gb AAK66966.1	histone H1 [Bufo bufo gargarizans]	29	14	
gi 4885513 ref NP_005373.1	neurofilament 3 (150kDa medium)...	28	19	
gi 6003540 gb AAF00492.1	neurofilament-3 (150 kD medium) [...	28	19	
gi 42523806 ref NP_969186.1	conserved hypothetical protein...	28	19	
gi 423935 pir A46194	neurofilament protein NF-220, high-mo...	28	19	
gi 45682130 ref ZP_00193566.1	COG1250: 3-hydroxyacyl-CoA d...	28	19	
gi 30466260 ref NP_848668.1	breast cancer 1, early onset [...	27	35	
gi 20808711 ref NP_623882.1	Sugar-binding periplasmic prot...	27	35	
gi 47530684 ref YP_022033.1	conserved hypothetical protein...	27	35	
gi 30023179 ref NP_834810.1	hypothetical protein [Bacillus...	27	35	
gi 13195201 gb AAK15600.1	BRCA1 [Bos taurus]	27	35	
gi 21225819 ref NP_631598.1	putative solute binding lipopr...	27	35	
gi 30265170 ref NP_847547.1	lipoprotein, putative [Bacillu...	27	35	
gi 121922 sp P06893 H1B_XENLA	HISTONE H1B >gi 2118972 pir ...	27	35	
gi 70670 pir HSXL1B	histone H1B - African clawed frog	27	35	
gi 13235457 emb CAC33750.1	Guanosine-3,5-bis(diphosphate) ...	27	46	
gi 7160454 emb CAB71173.2	calpastatin [Xenopus laevis]	27	46	
gi 13235476 emb CAC33635.1	Guanosine-3,5-bis(diphosphate) ...	27	46	
gi 42453561 ref ZP_00153468.1	hypothetical protein Rick041...	27	46	
gi 34580646 ref ZP_00142126.1	hypothetical (p)ppGpp 3-pyro...	27	46	
gi 15892349 ref NP_360063.1	similarity to (p)ppGpp 3-pyrop...	27	46	
gi 39595873 emb CAE67376.1	Hypothetical protein CBG12854 [...	27	46	
gi 14599407 emb CAC43460.1	probable major surface glycopro...	27	46	
gi 47228946 emb CAG09461.1	unnamed protein product [Tetrao...	27	46	
gi 7160452 emb CAB62094.2	calpastatin, putative [Xenopus l...	27	46	
gi 42526504 ref NP_971602.1	lipoprotein, putative [Trepone...	27	46	
gi 38085027 ref XP_112637.4	similar to KIAA0819 protein [M...	27	62	
gi 8163668 gb AAF73792.1	surface protein PspC [Streptococc...	27	62	

gi 8163642 gb AAF73778.1	surface protein PspC [Streptococc...	27	62
gi 6469853 gb AAF13459.1	unknown [Streptococcus pneumoniae]	27	62
gi 8163676 gb AAF73796.1	surface protein PspC [Streptococc...	27	62
gi 8163720 gb AAF73822.1	surface protein PspC [Streptococc...	27	62
gi 8163657 gb AAF73786.1	surface protein PspC [Streptococc...	27	62
gi 2981173 gb AAC06245.1	neurofilament medium subunit [Ser...	27	62
gi 8163695 gb AAF73807.1	surface protein PspC [Streptococc...	27	62
gi 121918 sp P06892 H1A_XENLA	HISTONE H1A >gi 64775 emb CAA...	27	62
gi 2511705 emb CAA71783.1	sigA binding protein [Streptococ...	27	62
gi 38085577 ref XP_359324.1	similar to KIAA0819 protein [M...	27	62
gi 8163701 gb AAF73810.1	surface protein PspC [Streptococc...	27	62
gi 46433713 gb EAK93144.1	hypothetical protein Ca019.6126 ...	27	62
gi 8163680 gb AAF73798.1	surface protein PspC [Streptococc...	27	62
gi 21398433 ref NP_654418.1	hypothetical protein predicted...	27	62
gi 15901997 ref NP_346601.1	choline binding protein A [Str...	27	62
gi 128146 sp P16053 NFM_CHICK	Neurofilament triplet M prote...	27	62
gi 70669 pir HSXL1A	histone H1A - African clawed frog	27	62
gi 14718664 gb AAK72978.1	choline-binding protein A CbpA [...	27	62
gi 14718658 gb AAK72975.1	choline-binding protein A CbpA [...	27	62
gi 63686 emb CAA29073.1	NF-M c-terminus [Gallus gallus]	27	62
gi 729671 sp P40280 H2A_MAIZE	Histone H2A >gi 7439704 pir ...	26	84
gi 31232261 ref XP_318672.1	ENSANGP00000010373 [Anopheles ...	26	84
gi 10720231 sp O80333 POR_MARPA	Protochlorophyllide reducta...	26	84
gi 45914575 ref ZP_0G196729.1	COG3422: Uncharacterized con...	26	84
gi 15239648 ref NP_200257.1	wound-responsive protein-relat...	26	84
gi 23027642 ref ZP_00066080.1	COG2207: AraC-type DNA-bindi...	26	84
gi 46188546 ref ZP_00124737.2	hypothetical protein Psyr021...	26	84
gi 39597796 emb CAE68488.1	Hypothetical protein CBG14291 [...	26	84
gi 5834783 emb CAB55338.1	hypothetical protein [Yarrowia l...	26	84
gi 19074182 ref NP_584788.1	hypothetical protein [Encephal...	26	112
gi 10437669 dbj BAB15083.1	unnamed protein product [Homo s...	26	112
gi 34870062 ref XP_221810.2	similar to CD209 antigen; dend...	26	112
gi 12858661 dbj BAB31400.1	unnamed protein product [Mus mu...	26	112
gi 13384730 ref NP_079640.1	RIKEN cDNA 1110005A23 [Mus mus...	26	112
gi 47198672 emb CAF93883.1	unnamed protein product [Tetrao...	26	112
gi 33667044 ref NP_056244.2	tarsh protein [Homo sapiens] >...	26	112
gi 45199188 ref NP_986217.1	AFR669Wp [Eremothecium gossypi...	26	112
gi 21357739 ref NP_651601.1	CG5520-PA [Drosophila melanoga...	26	112

# Alignments

Get selected sequences

Select all

Deselect all

☒ >gi|601931|gb|AAA57153.1| neurofilament-H  
Length = 511

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 348 AKSPVKEEAKSPEKAK 363

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 328 AKSPVKEEAKSPEKAK 343

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 308 AKSPVKEEAKSPEKAK 323

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 294 AKSPVKEEAKSPEKAK 309

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 274 AKSPVKEEAKSPEKAK 289

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 260 AKSPVKEEAKSPEKAK 275

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 240 AKSPVKEEAKSPEKAK 255

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16

AKSPVKEEAKSPEKAK

Sbjct: 226 AKSPVKEEAKSPEKAK 241

Score = 50.7 bits (112), Expect = 3e-06  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSPVKEEAKSPEKAK  
Sbjct: 128 AKSPVKEEAKSPEKAK 143

Score = 45.2 bits (99), Expect = 2e-04  
Identities = 14/14 (100%), Positives = 14/14 (100%)

Query: 1 AKSPVKEEAKSPEK 14  
AKSPVKEEAKSPEK  
Sbjct: 362 AKSPVKEEAKSPEK 375

Score = 45.2 bits (99), Expect = 2e-04  
Identities = 15/16 (93%), Positives = 15/16 (93%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSP KEEAKSPEKAK  
Sbjct: 194 AKSPEKEEAKSPEKAK 209

Score = 45.2 bits (99), Expect = 2e-04  
Identities = 15/16 (93%), Positives = 15/16 (93%)

Query: 1 AKSPVKEEAKSPEKAK 16  
AKSP KEEAKSPEKAK  
Sbjct: 180 AKSPEKEEAKSPEKAK 195

Score = 44.3 bits (97), Expect = 3e-04  
Identities = 16/22 (72%), Positives = 16/22 (72%), Gaps = 6/22 (27%)

Query: 1 AKSPVKE-----EAKSPEKAK 16  
AKSPVKE EAKSPEKAK  
Sbjct: 160 AKSPVKEEAKSPAEEAKSPEKAK 181

Score = 41.8 bits (91), Expect = 0.002  
Identities = 14/16 (87%), Positives = 15/16 (93%)